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bZIP transcription factors in the regulatory networks controlling seed maturation and germination of *Arabidopsis thaliana*

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ABSTRACT:

Temporal and tissue-specific expression of genes encoding Seed Storage Proteins (SSPs) is essential for a proper progression of developmental phases of the *Arabidopsis thaliana* seed maturation. Upon seed germination, the loosening of the endosperm cell walls (CWs), that is a crucial step for germination *sensu stricto* to occur, implicates several hydrolytic enzymes such as endo- β -mannanases (MAN; EC. 3.2.1.78; 1). Other hydrolytic enzymes such as Cathepsin B-like proteases (Cath B-like) are also important not only during germination *sensu stricto* but also in the early post-germination stages when reserve mobilization occurs (2, 3).

In all these processes, several bZIP Transcription Factors (TFs) are involved in controlling temporal and tissue-specific expression of seed genes. In the maturation phase, bZIPs, 10, 25 of the C-group (4) and bZIP53 of the S1-group participate in the formation of protein complexes that promote a drastic increase of the albumin 2S2 gene expression (5, 6). During seed germination, AtbZIP44 (S1-group) transcriptionally activates the AtMAN7 expression at the micropylar endosperm, allowing the radicle protrusion through this embryo-surrounding tissue (2). More recently, the G-Box Binding Factor 1 (GBF1; G-group) has been identified as a transcriptional repressor of the AtCathB3 gene expression at the radicle during seed germination (3).

The transcriptional combinatorial network through which these bZIPs regulate gene expression during the two phases of seed development (maturation and germination) has been explored. In the yeast 2-hybrid system, using as a bait AtbZIP44 and as a prey, an arrayed yeast library of circa 1,200 TF Open Reading Frames (TF ORFs) from *Arabidopsis thaliana* (7), the interaction between AtbZIP44 with other TFs such as those belonging to the C-group (AtbZIP9, AtbZIP10, AtbZIP25), the G-group (GBF1) or to other TF families has been further established, and its physiological significance investigated by several molecular techniques.

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(5) Alonso et al. (2009) *Plant Cell* 21: 1747-1761.

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(7) Castrillo et al. (2011) *PLoS One* 6: e21524.